

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/991,143DATE: 07/23/98
TIME: 14:43:16

INPUT SET: S27646.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Conti-Fine, B.M.
6
7 (ii) TITLE OF INVENTION: PREVENTION OF EXPERIMENTAL MYASTHANIA GRAVIS
8
9 (iii) NUMBER OF SEQUENCES: 2
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
13 (B) STREET: 121 South Eighth Street, 1600 TCF Tower
14 (C) CITY: Minneapolis
15 (D) STATE: MN
16 (E) COUNTRY: USA
17 (F) ZIP: 55402
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette
21 (B) COMPUTER: IBM Compatible
22 (C) OPERATING SYSTEM: Windows 95
23 (D) SOFTWARE: FastSEQ for Windows Version 2.0b
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 08/991,143
27 (B) FILING DATE: 16-DEC-1997
28 (C) CLASSIFICATION:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33
34
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Embretson, Janet E
38 (B) REGISTRATION NUMBER: 39,665
39 (C) REFERENCE/DOCKET NUMBER: 600.423US1
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 612-373-6959
43 (B) TELEFAX: 612-339-3061
44 (C) TELEX:
45
46

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47 (2) INFORMATION FOR SEQ ID NO:1:
48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1667 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: cDNA

56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58
59 AAGCACAGGC CACCACTCTG CCCTGGTCCA CACAAGCTCC GGTAGCCCAT GGAGCCCTGG 60
60 CCTCTCCTCC TGCTCTTTAG CCTTTGCTCA GCTGGCCTCG TCCTGGGCTC CGAACATGAG 120
61 ACCCGTCTGG TGGCAAAGCT ATTTAAAGAC TACAGCAGCG TGGTGC GGCC AGTGGAAGAC 180
62 CACCGCCAGG TCGTGGAGGT CACCGTGGGC CTGCAGCTGA TACAGCTCAT CAATGTGGAT 240
63 GAAGTAAATC AGATCGTGAC AACCAATGTG CGTCTGAAAC AGCAATGGGT GGATTACAAC 300
64 CTAATAATGGA ATCCAGATGA CTATGGCGGT GTGAAAAAAA TTCACATTCC TTCAGAAAAG 360
65 ATCTGGCGCC CAGACCTTGT TCTCTATAAC AATGCAGATG GTGACTTTGC TATTGTCAAG 420
66 TTCACCAAAG TGCTCCTGCA GTACACTGGC CACATCACGT GGACACCTCC AGCCATCTTT 480
67 AAAAGCTACT GTGAGATCAT CGTACCCAC TTTCCCTTTG ATGAACAGAA CTGCAGCATG 540
68 AAGCTGGGCA CCTGGACCTA CGACGGCTCT GTCTGGCCA TCAACCCGGA AAGCGACCAG 600
69 CCAGACCTGA GCAACTTCAT GGAGAGCGGG GAGTGGGTGA TCAAGGAGTC CCGGGGCTGG 660
70 AAGCACTCCG TGACCTATTC CTGCTGCCCC GACACCCCT ACCTGGACAT CACCTACCAC 720
71 TTCGTCATGC AGCGCCTGCC CCTCTACTTC ATCGTCAACG TCATCATCCC CTGCCTGCTC 780
72 TTCTCCTTCT TAACTGGCCT GGTATTCTAC CTGCCCACAG ACTCAGGGGA GAAGATGACT 840
73 CTGAGCATCT CTGTCTTACT GTCTTTGACT GTGTTCCCTT TGGTCATCGT GGAGCTGATC 900
74 CCCTCCACGT CCAGTGCTGT GCCCTTGATT GGAAAATACA TGCTGTTCAC CATGGTGTTC 960
75 GTCATTGCCT CCATCATCAT CACTGTCATC GTCATCAACA CACACCACCG CTCACCCAGC 1020
76 ACCCATGTCA TGCCCAACTG GGTGCGGAAG GTTTTTATCG ACACTATCCC AAATATCATG 1080
77 TTTTTCTCCA CAATGAAAAG ACCATCCAGA GAAAAGCAAG ACAAAAAGAT TTTTACAGAA 1140
78 GACATTGATA TCTCTGACAT TTCTGGAAAG CCAGGGCCTC CACCCATGGG CTTCCTACTC 1200
79 CCCCTGATCA AACACCCCGA GGTGAAAAGT GCCATCGAGG GCATCAAGTA CATCGCAGAG 1260
80 ACCATGAAGT CAGACCAGGA GTCTAACAAT GCGGCGGCAG AGTGGAAGTA CGTTGCAATG 1320
81 GTGATGGACC ACATACTCCT CGGAGTCTTC ATGCTTGTTC GCATCATCGG AACCTAGCC 1380
82 GTGTTTGCAG GTCGACTCAT TGAATTAAAT CAGCAAGGAT GAGCAGAAAA TGAGCTGAGC 1440
83 TTAGCTCTGC CCTGGAACCT ACCAGAGCAG AGAAGGGCAG GAGAGGAAGA TTTGTCTACT 1500
84 TGCTCCACTC GCACTTATCA AACGTGTTAT ATTCCATACT TATTATTGAT GATAAGATTT 1560
85 ACCTTTATGT AAGTTTATGG CTTGAAAGTG TTTTCATATT GCTTCTCCCT TTAGTTCTGC 1620
86 TGTCTCCCTG AAGAGTGAAC CCTCTTTAGT AAATGAACT AATCACT 1667

87

88 (2) INFORMATION FOR SEQ ID NO:2:

89

90 (i) SEQUENCE CHARACTERISTICS:

91 (A) LENGTH: 457 amino acids

92 (B) TYPE: amino acid

93 (C) STRANDEDNESS: single

94 (D) TOPOLOGY: linear

95

96 (ii) MOLECULE TYPE: protein

97

98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

99

RAW SEQUENCE LISTING PATENT APPLICATION US/08/991,143

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100 Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala Gly
101 1 5 10 15
102 Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe
103 20 25 30
104 Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val
105 35 40 45
106 Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp
107 50 55 60
108 Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp
109 65 70 75 80
110 Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys
111 85 90 95
112 Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu
113 100 105 110
114 Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val
115 115 120 125
116 Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe
117 130 135 140
118 Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln
119 145 150 155 160
120 Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val
121 165 170 175
122 Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
123 180 185 190
124 Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val
125 195 200 205
126 Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His
127 210 215 220
128 Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile
129 225 230 235 240
130 Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro
131 245 250 255
132 Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser
133 260 265 270
134 Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser
135 275 280 285
136 Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe
137 290 295 300
138 Val Ile Ala Ser Ile Ile Thr Val Ile Val Ile Asn Thr His His
139 305 310 315 320
140 Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe
141 325 330 335
142 Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro
143 340 345 350
144 Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile
145 355 360 365
146 Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser
147 370 375 380
148 Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys
149 385 390 395 400
150 Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala
151 405 410 415
152 Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly

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153          420          425          430
154    Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
155          435          440          445
156    Arg Leu Ile Glu Leu Asn Gln Gln Gly
157          450          455

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PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text